REMARKS

Reconsideration and withdrawal of the rejections of the application are requested in view of the a remarks herewith, which place the application into condition for allowance.

Examiner Canella and SPE Eyler are thanked for their helpful suggestions and courtesies extended during a telephone interview on April 1, 2004.

I. STATUS OF CLAIMS AND FORMAL MATTERS

Claims 65-83 and 90-105 are pending in this application. Claims 65, 66, 68, 69, 72, 73, 75, 77, 79, 80, 83 and 90 are amended; claims 91-105 are added.

Support for the amendments is found throughout the specification. Particular support for the recitation in claims 65, 66, 73, 75, 77, 79, 80, 83 and 90, regarding the location on the antibody of the first species to which the bifunctional molecule is bound, can be found on page 9, lines 24-28, of the specification. Support for claim 91 can be found in claim 65. Support for the bifunctional molecule binding to the constant region in claims 92-105 can be found in Figures 3 and 4, which depict the bifunctional molecule bound to the constant domain of the antibody of the first species. While there is no antecedent basis for "the constant domain", Applicants submit that this phrase is not indefinite because anyone skilled in the art would understand what the constant domain of an antibody is. Support for the non-naturally occurring group being biotin in claims 103 and 104 can be found in claim 74 and in the Examples. No new matter is added.

It is submitted that the claims, herewith and as originally presented, are patentably distinct over the prior art cited by the Examiner, and that these claims are and were in full compliance with the requirements of 35 U.S.C. §112. The amendments of and additions to the claims, as presented herein, are not made for purposes of patentability within the meaning of 35 U.S.C. §§§§ 101, 102, 103 or 112. Rather, these amendments and additions are made simply for clarification and to round out the scope of protection to which Applicants are entitled. Furthermore, it is explicitly stated that the herewith amendments should not give rise to any estoppel, as the herewith amendments are not narrowing amendments.

II. SUMMARY OF THE INVENTION

The following explanation is offered in an effort to provide the Examiner with a clearer understanding of the invention.

The instant invention provides a complex formed between an antibody or biologically active fragment of an antibody, from a first species, and a bifunctional molecule having a binding region of non-antibody origin and a constant region of an antibody from a second species. The complex is designed so that the antigen-binding or variable region of the antibody of the first species is available to bind its specific antigen, without hindrance due to the binding of the bifunctional molecule to the antibody (or a non-naturally occurring group provided thereon).

It would be clear to a skilled artisan from reading the specification as a whole that one purpose of the complex of the present claims is to function as a positive control in a diagnostic ELISA assay for detecting a given disease agent. In a preferred embodiment, the positive control complex of the invention mimics antibodies from human sera that are reactive with the disease agent. This approach involves the generation of a non-human antibody, such as a murine antibody, which binds to an antigen of the disease agent, and the subsequent labeling of this murine antibody with human constant domains. In other words, the murine antibody is labeled with human constant domains so that the murine antibody "looks like" a human antibody to the secondary capture antibody used in the ELISA assay. The advantage of this approach is that it avoids the need to obtain positive control reagents from human subjects.

In order to attach the human constant domain to the murine antibody (the "antibody from a first species"), a bifunctional molecule is prepared in which the constant region is linked to a binding region of non-antibody origin. The purpose of the binding region is to bind the mouse antibody, and thereby label the mouse antibody with human constant domains ("from an antibody of a second species"). It would be clear to a skilled artisan that it is important that the bifunctional molecule does not label the mouse antibody in the region of its paratope (*i.e.* antigen binding site), as this would interfere with the ability of the mouse antibody to detect the disease agent in the ELISA assay. The amendment to the independent claims made herein makes this concept even clearer. Specific support for the newly added language in claim 65 *et al.* is found on page 9, lines 24-28, where it states: "In a particularly preferred embodiment of the ninth aspect of the present invention, the bifunctional molecule is bound to a location on the antibody (or fragment thereof) of the first species which does not significantly hinder the binding between the antibody (or fragment thereof) and its specific antigen."

III. THE REJECTIONS UNDER 35 U.S.C. §112, 2ND PARAGRAPH, ARE OVERCOME

Claims 65-83 and 90 were rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. The rejections are traversed.

Claims 65, 66, 69, 73, 75, 77, 79, 80, 83 and 90 were rejected because "derived from" is allegedly unclear. The Examiner is reminded that the test for definiteness under the second paragraph of 35 U.S.C. §112 is whether "those skilled in the art would understand what is claimed when the claim is read in light of the specification." *Orthokinetic, Inc. v. Safety Travel Chairs, Inc.*, 806 F.2d 1565, 1576, 1 USPQ2d 1081, 1088 (Fed. Cir. 1986). Applicants submit that the meaning of this term is clear, both from its use in the specification and its ordinary meaning. Nonetheless, in the interest of expediting an already lengthy prosecution, the word "derived" has been removed from the claims, obviating the rejection on this basis.

The Office Action goes on to object to the recitation "biologically active fragment", apparently alleging that it is unclear which of numerous biological activities such a fragment should have. It is not at all unclear if one refers to page 7, lines 25-27, which states: "By 'biologically active fragment' we mean a fragment which mimics the binding of the antibody derived from the first species to at least one antigenic determinant."

Claim 72 has been amended to address the question regarding "a histidine rich protein". The "a" has been removed, to clarify that the claim refers to "the" histidine rich protein described by Borza *et al.* in rabbit, and by Gorgani *et al.* in human, and to homologues of histidine rich protein that may be isolated from other species.

In view of the foregoing, reconsideration and withdrawal of the rejections under 35 U.S.C. §112, second paragraph, are requested.

IV. THE REJECTIONS UNDER 35 U.S.C. §112, 1ST PARAGRAPH ARE OVERCOME

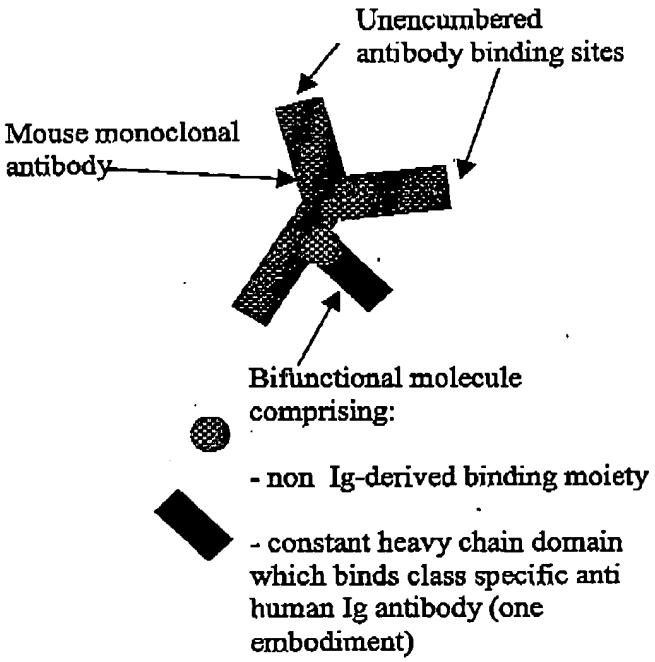
Claims 65-68, 72-83 and 90 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking adequate written description. The rejection is traversed.

(A) As drawn to complexes comprising a bifunctional molecule comprising a binding region of non-antibody origin.

It appears as though a main concern regarding this point is that there are no structural or functional attributes to the binding region of the bifunctional molecule because it can bind to the paratope of the antibody of the first species. The herein amendments have modified the claims to clarify that a binding region that binds to the paratope of the antibody of the first species is

excluded from the scope of the claims. As discussed in the Summary of Invention, above, a binding region that hinders the antibody of the first species from binding to its antigen by binding to the paratope would be counter to the aim of the invention.

The comments on page 4 of the Office Action indicate that the present invention is misunderstood. In particular, the Office Action notes that the epitopes of the infectious disease agents recited in the specification would bind to the antibody paratope, rather than the antibody constant region. It is true that the epitopes of the infectious disease agents would bind to the paratope of the antibody of the first species. However, this has nothing to do with where the binding region of the bifunctional molecule binds to the antibody of the first species (or to a non-naturally occurring group provided thereon). In fact, it is **preferred** (and now required by the claim language) that the bifunctional molecule does not bind to the paratope of the antibody of the first species, so that the paratope is left clear to bind to epitopes of infectious disease agents. The figure below depicts an embodiment of the claimed invention, and should clear up any remaining confusion with respect to which elements of the claimed complex bind what moieties.



(B) As drawn to binding regions "derived from" protein A, protein G or protein L and to constant regions "derived from" an antibody of a second species.

The Office Action raises concerns that the specification fails to provide written description for binding regions "derived from" protein A, G or L. A similar concern is raised regarding constant regions "derived from" an antibody of a second species. In particular, the Office Action states that the claims encompass derivatives of protein A, G, L and constant regions which encompass deletions, additions and substitutions to the amino acid sequence as well as other non protein modifications. To the contrary, representative modifications are disclosed in the specification, and several of them are summarized on page 5 of the Office Action. Furthermore, functional binding language is recited in the claims, excluding any members of the genus that do not perform as claimed. However, as discussed above, the word "derived" has been removed from the claims, addressing the concern that the claims encompass deletions, additions and substitutions to the amino acid sequence of the recited proteins. The claims do, however, encompass fragments, and these are supported by the specification, and by the knowledge in the art at the time the application was filed.

Indeed, protein A, protein G and protein L were well known at the time the present application was filed, and binding fragments of these proteins had been well characterized as well. (See, for example, the attached abstracts of references relating to proteins A and G, and U.S. Patent No. 4,876,194, which relates to fragments of protein L that bind to immunoglobulins.

The skilled artisan would understand that the concept behind the invention is to "tag" or "label" an antibody of, for example, murine origin, with a constant region of, for example, a human antibody. This "tagging" or "labelling" is achieved by fusing the human constant region to a binding region derived from a protein capable of binding to the murine antibody. A skilled artisan would also understand that, as the complex is to be used as a positive control in an ELISA assay, it is important to keep the paratope of the murine antibody free so that it can bind with the epitopes of the disease agent in the ELISA assay. A skilled artisan would therefore understand that a number of modifications can be made to the binding region of the bifunctional molecule, provided that the modified region retains the ability to bind to the murine antibody in a region away from the paratope of the murine antibody.

(C) As drawn to a bifunctional molecule comprising a histidine rich glycoprotein

As discussed above, the recitation of "histidine rich glycoprotein" is intended to refer to the proteins described by Borza *et al* and Gorgani *et al*, and to homologues in species other than rabbit and human. Therefore, this aspect of the rejection is overcome by the amendment to claim 72.

Claims 65-83 and 90 were rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking enablement. This rejection is traversed, for reasons discussed in detail above. The skilled artisan would be able to make and use the invention, based solely on the disclosure of the application and his or her own knowledge of the art, with no undue experimentation.

Reconsideration and withdrawal of the rejections under the first paragraph of 35 U.S.C. §112 are requested.

V. THE REJECTIONS UNDER 35 U.S.C. §102 ARE OVERCOME

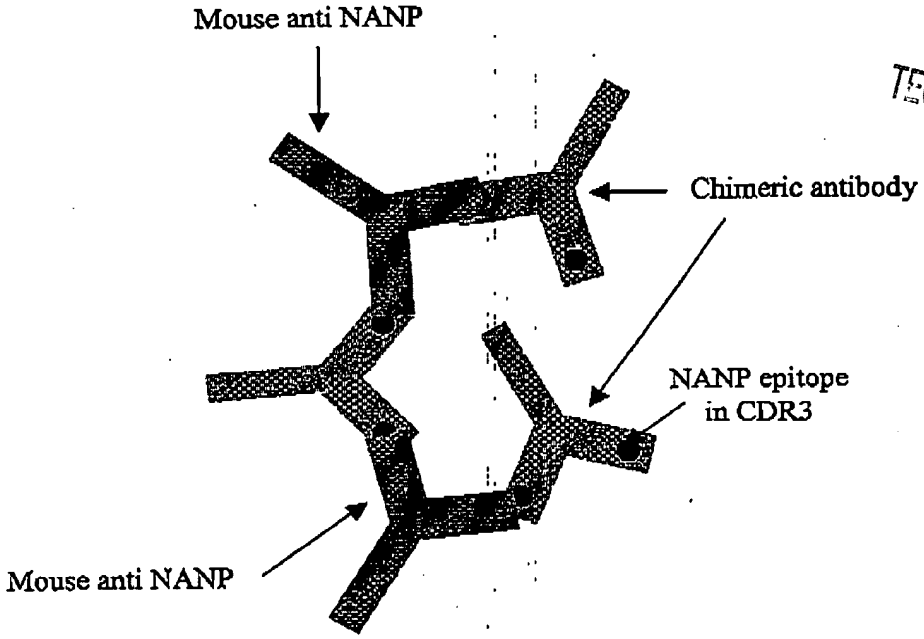
Claims 66, 67, 73 and 77 were rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Zanetti *et al*. The rejection is traversed.

As has been explained and discussed numerous times throughout prosecution of this application, Zanetti describes a complex between :

i) a mouse monoclonal antibody [Sp-3-B4] directed against the $(NANP)_3$ epitope from *Plasmodium falciparum*; and

ii) an engineered antibody [y1NANP] to which the $(NANP)_3$ epitope has been introduced as a foreign epitope into the CDR3 region of the mouse/human chimera CK_161.

The Zanetti complex is depicted below.



In order to arrive at the conclusion of anticipation, the Examiner must consider the mouse monoclonal Sp-3-B4 antibody of Zanetti to be equivalent to the "antibody or biologically active fragment thereof derived from a first species" as recited in the present claims. It follows that the Examiner must also consider the y1NANP antibody to be equivalent to the bifunctional molecule with the $(NANP)_3$ epitope as the "binding region of non-antibody origin".

This is clearly a strained interpretation of the present claims and the Zanetti reference. It would be clear to a skilled artisan from a reading of the specification as a whole that the purpose of the complex of the present claims is to function as a positive control in a diagnostic ELISA assay for detecting a given disease agent. As discussed above, this approach involves, for example, the generation of murine antibodies which bind to an antigen of the disease agent, and subsequent labeling of this murine antibody with human constant domains. In order to attach the human constant domain to the mouse antibody, a bifunctional molecule is prepared in which the constant region is linked to a binding region of non-antibody origin. The purpose of the binding region is to bind the mouse antibody and thereby label the mouse antibody with human constant domains. It would be clear to a skilled artisan that it is important that the bifunctional molecule

does not label the mouse antibody in the region of its paratope, as this would interfere with the ability of the mouse antibody to detect the disease agent in the ELISA assay.

In the Zanetti complex, however, the y1NANP antibody binds directly to the paratope of the mouse SP-3-B4 antibody. For this reason, the mouse SP-3-B4 antibody could not function as a positive control in an ELISA assay. A skilled artisan would understand that the Zanetti citation does not in a any way teach the same invention as that claimed in the present application.

In any case, Applicants believe that newly added claim language regarding the bifunctional molecule being bound to a location on the antibody of the first species that does not significantly hinder the binding between the antibody and its specific antigen, even more clearly distinguishes the present claims from the Zanetti citation.

Claims 65-68, 77, 78, 81-83 and 90 were rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Lynch *et al.* The rejection is traversed.

Contrary to the statements on page 9 of the Office Action, Lynch discloses a bifunctional molecule where human Fas (not human Fas ligand) is fused to the constant region of human IgG1. Its sole purpose is to provide a molecule against which anti-Fas monoclonal antibodies can be produced, and subsequently easily purified by complexing with the huFas-Fc construct, followed by affinity chromatography on immobilized Protein A. The nature of the interaction between the huFas-Fc construct and the anti-Fas mouse monoclonal antibody is a normal antigen-antibody interaction via the antibody paratope in the V region of the mAb.

Once again, the language added to the claims (*i.e.* that the bifunctional molecule is bound to a location on the antibody of the first species that does not significantly hinder the binding between the antibody and its specific antigen) provides further clarification of the distinction between the present claims and the Lynch reference.

Accordingly, reconsideration and withdrawal of the rejections under 35 U.S.C. §102 are believed to be in order and such action is requested.

VI. THE REJECTIONS UNDER 35 U.S.C. §103 ARE OVERCOME

Claims 65-68, 77, 78, 81-83 and 90 were rejected under 35 U.S.C. §103(a) as allegedly being unpatentable over Lynch *et al.* in view of Chang *et al.* The rejection is traversed.

As discussed above, Lynch does not teach or suggest the instant invention. Chang does nothing to remedy the deficiencies of Lynch, as it relates only to peptide linkers, and not to antibody-bifunctional molecule complexes for use in assays. As the Examiner is aware, each and

every claim limitation must be taught by the combination of references for a Section 103 rejection to be proper, and that burden has not been met here.

Claims 65-70, 77, 78 and 81 were rejected under 35 U.S.C. §103(a) as allegedly being unpatentable over the abstract of Sekisui-Chem, in view of Lynch *et al*. The rejection is traversed.

The rejection is based on the Examiner's interpretation that the abstract of Sekisui-Chem teaches a bifunctional molecule comprising protein A linked via a relatively short linker peptide to the Fc region of IgG (see the paragraph bridging pages 10 and 11 of the Office Action). This interpretation, however, is incorrect. Indeed, the translation of the abstract relied on by the Examiner is quite misleading. The abstract refers to a "gene encoding a region of Protein A for fusion with Fc". It also states: "These terminal regions allow the fusion of protein-A with the Fc". In fact, however, the protein A region is *not* fused with an Fc region of an IgG.

Enclosed is an abstract of this citation from the Derwent Innovation Index . This abstract clearly shows that the claimed molecule is the gene for fragment B of Protein A, linked via a linker peptide ("Z", length undeclared), to "X", which is an amino acid having a functional group to enable easy attachment to a solid support, *e.g.* cysteine, lysine, tyrosine *etc*.

This abstract does not in any way suggest that the Protein A fragment is fused to an Ig Fc region. In fact, the sole purpose of the disclosed molecule is to more readily immobilize Protein A on a solid support for the widely used practice of purifying IgGs, which bind to protein A. In other words, the claimed molecule is used to capture antibodies from a sample through the interaction of the Fc protein of antibodies in the sample with the protein A fragment. Notably, the Derwent abstract describes this in terms of a "protein A substance for combining Fc" (not for fusing with Fc).

As a further point, the Examiner is reminded that a cited reference must contain an enabling disclosure to be properly included in an art rejection. Applicants question whether the Sekisui Chem abstract meets this requirement. It is understood from the interview on April 1, 2004 with Examiner Canella and SPE Eyler that the full text of the Sekisui Chem reference will be obtained and translated by the USPTO to ascertain what the reference teachings are.

None of the cited references, alone or in combination, teach or suggest the presently claimed complexes. Therefore, reconsideration and withdrawal of the rejections under 35 U.S.C. §103 are requested.

CONCLUSION

In view of the remarks and amendments herewith, the application is believed to be in condition for allowance. Favorable reconsideration of the application and prompt issuance of a Notice of Allowance are earnestly solicited. The undersigned looks forward to hearing favorably from the Examiner at an early date.

Respectfully submitted,

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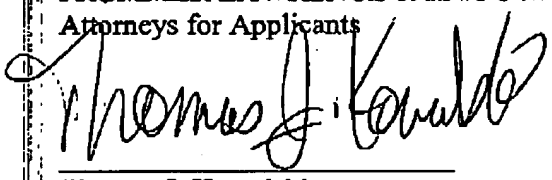
Attorneys for Applicants



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Eur J Biochem. 1986 May 2;156(3):637-43. Related Articles, Links

Staphylococcal protein A consists of five IgG-binding domains.

Moks T, Abrahmsen L, Nilsson B, Hellman U, Sjoquist J, Uhlen M.

A genetic approach is described to clarify the IgG-binding properties of the N-terminal portion of staphylococcal protein A (region E). Several gene fragments, encoding region E or B or protein A, have been cloned and expressed in Escherichia coli. The gene products were purified by IgG-affinity chromatography and subjected to structural and functional analyses. Both fragments can be efficiently purified using this method, suggesting that region B as well as region E has Fc-binding activity. In addition, gene fusions were assembled giving fragments EB and EE, which both showed a divalent Fc-binding. These results demonstrate that protein A consists of five IgG-binding domains. The implications of these findings for the structure of protein-A--immunoglobulin-G complexes are discussed.

PMID: 2938951 [PubMed - indexed for MEDLINE]

EMBO J. 1986 Jul;5(7):1567-75. Related Articles, Links

Structure of the IgG-binding regions of streptococcal protein G.

Guss B, Eliasson M, Olsson A, Uhlen M, Frej AK, Jornvall H, Flock JI, Lindberg M.

The gene encoding the IgG-binding protein G from streptococcus G148 was isolated by molecular cloning. A subclone containing a 1.5-kb insert gave a functional product in Escherichia coli. Protein analysis of affinity-purified polypeptides revealed two gene products, both smaller than protein G spontaneously released from streptococci, but with identical IgG-binding properties. The complete nucleotide sequence of the insert revealed a repeated structure probably evolved through duplications of fragments of different sizes. The deduced amino acid sequence revealed an open reading frame extending throughout the insert, terminating in a TAA stop codon. Analysis of the two gene products by N-terminal amino acid determination suggests that two different TTG codons are recognized in E. coli for initiation of translation to yield the two products. Based on these results several truncated gene constructions were expressed and analysed. The results suggest that the C-terminal part of streptococcal protein G consists of three IgG-binding domains followed by a region which anchors the protein to the cell surface. Structural and functional comparisons with streptococcal M protein and staphylococcal protein A have been made.

PMID: 3017704 [PubMed - indexed for MEDLINE]

J Bacteriol. 1986 Sep;167(3):870-80. Related Articles, Links

Gene for an immunoglobulin-binding protein from a group G streptococcus.

Fahnestock SR, Alexander P, Nagle J, Filpula D.

The gene (spg) for an immunoglobulin G (IgG)-binding protein from a Streptococcus clinical isolate of Lancefield group G was cloned and expressed in Escherichia coli. The complete nucleotide sequence of the gene and 5'-flanking sequences was determined. The DNA sequence includes an open reading frame which encodes a hypothetical protein of 448 amino acid residues (Mr = 47,595). The 5' end of this open reading frame encodes a sequence resembling a typical secretion signal sequence, and the remainder of the encoded protein has features reminiscent of staphylococcal protein A and of streptococcal M6 protein, including repeated sequences and a similar C-terminal structure. Aside from this C-terminal structure, the encoded protein has little direct amino acid sequence homology to either protein A or M6 protein. In E. coli, the cloned gene directs the synthesis of a protein which binds to immunoglobulins, including rabbit immunoglobulin, goat IgG, and human IgG3(lambda). Its binding properties are similar to those of the protein G described by Bjorck and Kronvall (L. Bjorck and G. Kronvall, J. Immunol. 133:969-974, 1984), a type III Fc receptor from a group G streptococcus.

PMID: 3745123 [PubMed - indexed for MEDLINE]

J Biol Chem. 1987 Oct 5;262(28):13388-91. Related Articles, Links

Definition of IgG- and albumin-binding regions of streptococcal protein G.

Akerstrom B, Nielsen E, Bjorck L.

Department of Physiological Chemistry, University of Lund, Sweden.

Protein G, the immunoglobin G-binding surface protein of group C and G streptococci, also binds serum albumin. The albumin-binding site on protein G is distinct from the immunoglobulin G-binding site. By mild acid hydrolysis of the papain-liberated protein G fragment (35 kDa), a 28-kDa fragment was produced which retained full immunoglobulin G-binding activity (determined by Scatchard plotting) but had lost all albumin-binding capacity. A protein G (65 kDa), isolated after cloning and expression of the protein G gene in Escherichia coli, had comparable affinity to immunoglobulin G (5-10 X 10(10)M-1), but much higher affinity to albumin than the 35- and 28-kDa protein G fragments (31, 2.6, and 0 X 10(9)M-1, respectively). The amino-terminal aminoacid sequences of the 65-, 35-, and 28-kDa fragments allowed us to exactly locate the three fragments in an overall sequence map of protein G, based on the partial gene sequences published by Guss et al. (Guss, B., Eliasson, M., Olsson, A., Uhlen, M., Frej, A. K., Jonsson, L. R., Flock, J. I., and Lindberg, M. (1986) EMBO J. 5, 1567-1575) and Fahnestock et al. (Fahnestock, S. R., Alexander, P., Nagle, J., and Filpula, D. (1986) J. Bacteriol. 167, 870-880). In this map, could then be deduced the location of three homologous albumin-binding regions and three homologous immunoglobulin G-binding regions.

Figure shows reference to both Fahnestock [2 binding domains GX7809] and Guss references [3 binding domains for G148 Streptococcus Protein G]

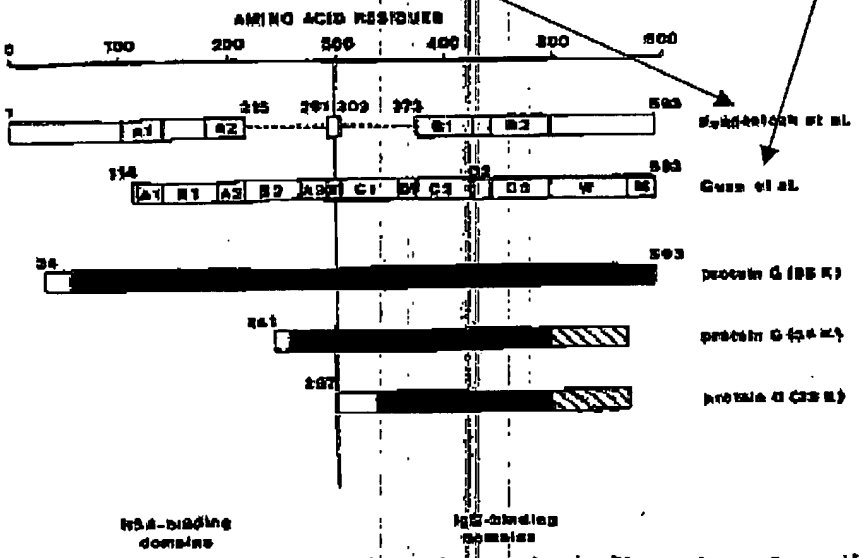

FIG. 5. **Molecular mapping of protein G.** Shown is a schematic drawing of the translated amino acid sequences from protein G-encoding genes described by Fahnestock *et al.* (13) and Guss *et al.* (12), and the amino acid sequences of the three protein G molecules described in this paper. Protein G(65K) is the product of a protein G gene cloned and expressed in *E. coli*; protein G(35K) was solubilized from streptococci by papain treatment, and protein G(28K) was a degradation product of the latter fragment, obtained by mild acid hydrolysis. *Open regions* designate known sequences, *solid regions* unknown sequences, and the *striated* sequences indicate that the site of papain cleavage for the solubilization of protein G(35K) and protein G(28K) is unknown. *Dotted lines* indicate deletions in the Fahnestock gene. This gene was from a different group G streptococcal strain than the three protein G molecules used here, which all originate from the G148 strain. The gene of Guss *et al.* was also from the G148 strain. The deduced amino acid sequences of Guss *et al.* and Fahnestock *et al.* are identical to each other where overlapping, and to the *open regions* of the protein G-fragments. The numbering of amino acids is based on the position of amino acid one at the initiation codon found in the Fahnestock gene. *A*, *B*, *C*, and *D* sequences indicate different homologous regions as suggested by the authors. *W* and *M* designate wall spanning and membrane anchoring regions, respectively, and at position 594 is found a stop codon. *HSA*, human serum albumin.

Patent Number(s):
JP1060388-A [SUPPLEMENT]

Title:
Gene encoding linker peptide of Fc binding region of protein A - with amino acid sequence with functional gps. which easily combine with solid carriers used to bind with IgG Fc, e.g. for diagnosis

Patent Assignee Name(s) and Code(s):
SEKISUI CHEM IND CO LTD (SEKI)

Derwent Primary Accession Number:
1989-318566 [44]

Abstract:
Gene for coding a combining body of a region of protein A substance for combining Fc is claimed. The combined body is a polypeptide which comprises combined aminoacid sequences constructing a region of protein A substance for combining Fc, a relatively short linker-polypeptide combining aminoacids, and aminoacid sequences which have functional gps. for easily combining with solid carriers and are added to at least N-terminal or C-terminal of aminoacid sequences. The region for combining Fc has the ability to cause protein A substance to combine with Fc region of Ig G.

The gene pref. has nucleotides for coding the following polyamino acid sequence (I)

(ADNKFNKEQQNA FYEILHLPNLNEE QRNGFIQSLKDD PSQSANLLAEAKK LNDAQAPK-Z)nX

, wherein n is integer and at least 2; X is aminoacid having a gp. for easily combining with a solid carrier, Z is linker-polypeptide, and A:alanine, Cy:cystein, D:asparagine acid, E:glutamic acid, F:phenylalanine, G:glycine, H:histidine, I:isoleucine, K:lysine; L:leucine, M:methionine, N:asparagine, P:proline, Q:glutamine, R:arginine, s:serine, Y:tyrosine.

The gene pref. comprises a specified nucleotide (II).

USE/ADVANTAGE - The body for combining with Fc of IgG can be useful as immune absorbent for various diagnosis and basic medical study; for removing anti-II factor antibody in haemophilia B and antinuclear antibody in SLE as well as for treatments of cancer. By this method, protein A substance having this body can be produced in high purificn. and yield without utilising dangerous microbes such as Staphylococcus.

International Patent Classification:
C12N-001/20; C12N-015/00; C12P-021/02; C12R-001/19

Derwent Class:
B04 (Natural products and polymers, testing, compounds of unknown structure); D16 (Fermentation industry)

Derwent Manual Code(s):
B04-B02B1; B04-B04A1; B04-B04A5; B04-B04C6; B04-C01G; B11-C07A; B12-G07; B12-K04A; D05-C11; D05-C12; D05-H03B; D05-H04; D05-H09; D05-H11; D05-H12

Patent Number	Publ. Date	Main IPC	Week	Page Count	Language
JP1060388-A	07 Mar 1989		198944	Pages: 27	

Abstract

PURPOSE:To provide a gene coding a linked substance composed of a polypeptide produced by linking a plurality of amino acid sequences constituting Fc bond region of a protein A-like substance through a relatively short linker peptide and constructed in such a manner as to be easily linkable with a solid phase carrier.

CONSTITUTION:The objective gene codes a linked substance composed of a polypeptide produced by linking a plurality of amino acid sequences constituting Fc bond region which is a part of protein A-like substance capable of bonding the Fc part of immunoglobulin through a relatively short linker peptide and added with an amino acid having functional group easily linkable with at least the N terminal or C terminal of the amino acid sequence. The linker peptide is preferably an amino acid having a functional group easily linkable with a solid carrier or a peptide containing an amino acid sequence which can be specifically cut by chemical or enzymatic treatment at a site adjacent to the above amino acid. A protein A-like substance which can be supported on a solid phase and can be easily purified is obtained in large quantity by the use of a transformant produced by the gene.